



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/766, 511  
Source: OIPE  
Date Processed by STIC: 2/5/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/766,511

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)      (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.  
AKS-Biotechnology Systems Branch- 5/15/99

OIPE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/766,511

DATE: 02/05/2001  
 TIME: 13:34:38

Input Set : A:\10147\_61.txt  
 Output Set: N:\CRF3\02052001\I766511.raw

*Does Not Comply  
 Corrected Diskette Needed  
 See Attachment  
 Last page*

```

3 <110> APPLICANT: MCCARTHY, Sean A
4 FRASER, Christopher C
5 SHARP, John D
6 BARNES, Thomas S
7 KIRST, Susan J
8 MYERS, Paul S
9 WRIGHTON, Nicholas
10 GOODEARL, Andrew
11 HOLTZMAN, Douglas A
12 KHODADOUST, Mehran M
14 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC,
15 DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER USES
17 <130> FILE REFERENCE: 210147.0065/65US
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/766,511
20 <141> CURRENT FILING DATE: 2001-01-19
22 <150> PRIOR APPLICATION NUMBER: US 09/578,063
23 <151> PRIOR FILING DATE: 2000-05-24
25 <150> PRIOR APPLICATION NUMBER: US 09/333,159
26 <151> PRIOR FILING DATE: 1999-06-14
28 <150> PRIOR APPLICATION NUMBER: US 09/596,194
29 <151> PRIOR FILING DATE: 2000-06-16
31 <150> PRIOR APPLICATION NUMBER: US 09/342,364
32 <151> PRIOR FILING DATE: 1999-06-29
34 <150> PRIOR APPLICATION NUMBER: US 09/608,452
35 <151> PRIOR FILING DATE: 2000-06-30
37 <150> PRIOR APPLICATION NUMBER: US 09/393,996
38 <151> PRIOR FILING DATE: 1999-09-10
40 <150> PRIOR APPLICATION NUMBER: US 09/345,680
41 <151> PRIOR FILING DATE: 1999-06-30
43 <160> NUMBER OF SEQ ID NOS: 85
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49 <212> TYPE: DNA
50 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/766,511  
 DATE: 02/05/2001  
 TIME: 13:34:39

Input Set : A:\10147\_61.txt  
 Output Set: N:\CRF3\02052001\I766511.raw

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66 caaqcacagc tctcttttcag gcccttccatg gactacaata tatgaactca cacttttgtct 840
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71 cagcagccga ctgagctgag cccagcaggt catctgctcc agcctgtcct ctcgtcaqcc 1140
72 ttctctctcc agaagctgtt gtagagacat tcaggagaga gcaagccctt tgcctgttt 1200
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78 tglcttctct ggaatcact gcccttccag ggcattctca ggcgggggg tclcttccc 1560
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113 tctacagagg actgctgtgg ctccaggtgc tgtgtgcggg cctctctcat acagaggtg 180
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RAW SEQUENCE LISTING                      DATE: 02/05/2001  
 PATENT APPLICATION: US/09/766,511        TIME: 13:34:39

Input Set : A:\10147\_61.txt  
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119 cctccqcccc cgtacgaaca ggtagtgaag gcccaag 516
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123 <211> LENGTH: 172
124 <212> TYPE: PRT
125 <213> ORGANISM: Homo sapiens
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132 20 25 30
134 Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
135 35 40 45
137 Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
138 50 55 60
140 Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
141 65 70 75 80
143 Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
144 85 90 95
146 Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
147 100 105 110
149 Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
150 115 120 125
152 Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
153 130 135 140
155 Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr
156 145 150 155 160
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163 <211> LENGTH: 22
164 <212> TYPE: PRT
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167 <400> SEQUENCE: 4
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171 Leu Glu Cys Thr Glu Ala
172 20
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177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 5
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182 1 5 10 15
184 Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg Cys Cys Val Arg Ala
185 20 25 30

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RAW SEQUENCE LISTING                      DATE: 02/05/2001  
 PATENT APPLICATION: US/09/766,511        TIME: 13:34:39

Input Set : A:\10147\_61.txt  
 Output Set: N:\CRF3\02052001\I766511.raw

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188      35      40      45
190 Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile Arg Arg Arg Met Tyr
191      50      55      60
193 Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn Val Ser Tyr Thr Arg
194      65      70      75      80
196 Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln Pro Gly Pro Pro Tyr
197      85      90      95
199 Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro Val Gly Asn Ser Met
200      100     105     110
202 Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro Gln Gly Ser Val Ala
203      115     120     125
205 Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro Pro Pro Pro Tyr Glu
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224 Leu Ser Ile Gln Arg Leu
225      35
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238      20
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251      20      25      30
253 Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
254      35      40      45
256 Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
257      50      55      60

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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/766,511

DATE: 02/05/2001  
 TIME: 13:34:39

Input Set : A:\10147\_61.txt  
 Output Set: N:\CRF3\02052001\1766511.raw

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279 <213> ORGANISM: Mus sp.
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*A HACHMENT*

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	130					135					140				
Gly	Asn	Gly	Lys	Trp	Gln	Trp	Ile	Asp	Asp	Thr	Pro	Phe	Ser	Gln	Asn
145					150					155					160
Val	Arg	Phe	Trp	His	Pro	His	Glu	Pro	Asn	Leu	Pro	Glu	Glu	Arg	Cys
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Val	Ser	Ile	Val	Tyr	Trp	Asn	Pro	Ser	Lys	Trp	Gly	Trp	Asn	Asp	Val
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Phe	Cys	Asp	Ser	Lys	His	Asn	Ser	Ile	Cys	Glu	Met	Lys	Lys	Ile	Tyr
	195						200					205			

Leu

<210> 61  
 <211> 821  
 <212> DNA  
 <213> Mus sp.

*see item #10 on ERROR SUMMARY  
 Report. Use of "n" requires numeric  
 identifiers <220>, <221>, <222>, and <223>.*

<400> 61  
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 gtgtgtggaa gttgattctg aactctggcc tctttgacag aagccaggtc cctgagtcgt 120  
 attttgaga cagatgcaag aaaccctga ccttctgaac atacacctca acaatggtgc 180  
 aggaaagaca atcccaaggg aaggagctct gctggaccct gagactctgg tcagctgctg 240  
 tgatttccat gttactcttg agtacctgtt tcattgagag ctgtgtggtg acttaccat 300  
 ttattatgga ccagcccagt agaagactat atgaacttca cacataccat tccagtctca 360  
 cctgcttcag tgaagggact atggtgtcag aaaaaatgtg gggatgctgc ccaaatact 420  
 ggaagtcatt tggctccagc tgctacctca tttctaccaa ggagaacttc tggagcacca 480  
 gtgagcagaa ctgtgttcag atgggggctc atctggtggt gatcaatact gaagcggagc 540  
 agaatttcat caccagcag ctgaatgagt cactttctta cttcctgggt ctttcggatc 600  
 ccaaggtat ggcaaattgc aatggatcga tgatactct ttcagtcaaa atgtcaggtt 660  
 ctggcaccce catgaaccca atcttccaga agagcgggtg gtttcaatag tttactggaa 720  
 tccttcgaaa tggggctggg aatgatgttt tctgtgatag taaacacaat tcaatatgtg 780  
 aatgaan<sup>0</sup> gattacctat gaatgcctgt tattcttaat a 821

<210> 62  
 <211> 534  
 <212> DNA  
 <213> Mus sp.

<400> 62  
 atggtgcagg aaagacaatc ccaagggaag ggagtctgct ggaccctgag actctggtca 60  
 gctgctgtga tttccatgtt actcttgagt acctgtttca ttgagagctg tgtggtgact 120  
 taccaattta ttatggacca gccagtaga agactatatg aacttcacac ataccattcc 180  
 agtctcacct gcttcagtga agggactatg gtgtcagaaa aaatgtgggg atgctgccca 240  
 aatcactgga agtcatttgg ctccagctgc tacctcattt ctaccaagga gaacttctgg 300  
 agcaccagtg agcagaactg tgttcagatg ggggctcatc tgggtggtgat caatactgaa 360  
 gcggagcaga atttcatcac ccagcagctg aatgagtcac tttcttactt cctgggtcct 420



## VERIFICATION SUMMARY

DATE: 02/05/2001

PATENT APPLICATION: US/09/766,511

TIME: 13:34:40

Input Set : A:\10147\_61.txt

Output Set: N:\CRF3\02052001\I766511.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number  
 L:267 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:268 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:  
 L:272 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:273 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:  
 L:391 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:392 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:  
 L:433 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:434 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:  
 L:438 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:439 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:  
 L:443 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:444 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:  
 L:448 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:449 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:  
 L:453 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:454 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:  
 L:1749 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1750 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:  
 L:1754 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1755 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE:  
 L:1896 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1897 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:  
 L:1901 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1902 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (45) SEQUENCE:  
 L:1906 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1907 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:  
 L:1911 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1912 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (47) SEQUENCE:  
 L:1916 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1917 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (48) SEQUENCE:  
 L:1921 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1922 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (49) SEQUENCE:  
 L:1926 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:1927 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (50) SEQUENCE:  
 L:2118 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:2119 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (56) SEQUENCE:  
 L:2123 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:2124 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (57) SEQUENCE:  
 L:2128 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:2129 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (58) SEQUENCE:  
 L:2133 M:283 W: Missing Blank Line separator, <400> field identifier  
 L:2134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (59) SEQUENCE:  
 L:2205 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61  
 L:2205 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:61  
 L:2205 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:61  
 L:2205 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:61  
 L:2205 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61

VERIFICATION SUMMARY                      DATE: 02/05/2001  
PATENT APPLICATION: US/09/766,511        TIME: 13:34:40

Input Set : A:\10147\_61.txt  
Output Set : N:\CRF3\02052001\1766511.raw

L:2322 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2323 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (66) SEQUENCE:  
L:2327 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2328 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (67) SEQUENCE:  
L:2332 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2333 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (68) SEQUENCE:  
L:2337 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2338 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (69) SEQUENCE:  
L:2342 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2343 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (70) SEQUENCE:  
L:2513 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2514 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (74) SEQUENCE:  
L:2518 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2519 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (75) SEQUENCE:  
L:2523 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2524 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (76) SEQUENCE:  
L:2528 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2529 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (77) SEQUENCE:  
L:2533 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2534 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (78) SEQUENCE:  
L:2538 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2539 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (79) SEQUENCE:  
L:2543 M:283 W: Missing Blank Line separator, <400> field identifier  
L:2544 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (80) SEQUENCE: